

SEQUENCE LISTING

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OKUDA, MITSUYOSHI
SAEKI, KATSUHISA
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HITOMI, JUN
KAGEYAMA, YASUSHI
SHIKATA, SHITSUW
NOMURA, MASAFUMI

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<141> 2000-04-06

<150> PCT/JP98/04528

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His	Asp	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met	Ala	Thr	Pro		
	450					455					460						
att	gtt	gcg	ggg	aat	gtt	gca	cag	ctc	cgt	gag	cat	ttt	gtg	aaa	aat	1440	
Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe	Val	Lys	Asn		
465					470				475						480		
aga	gga	atc	act	cct	aag	cct	tcc	cta	ttg	aaa	gca	gct	ttg	att	gca	1488	
Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	Leu	Leu	Lys	Ala	Ala	Leu	Ile	Ala		
				485				490						495			
ggt	gct	gct	gat	gtt	gga	ttg	ggt	tat	ccg	aac	gga	aac	caa	gga	tgg	1536	
Gly	Ala	Ala	Asp	Val	Gly	Leu	Gly	Tyr	Pro	Asn	Gly	Asn	Gln	Gly	Trp		
			500				505						510				
ggc	cga	gtg	acc	ctg	gat	aaa	tcg	ttg	aac	gtt	gcc	tat	gtg	aac	gaa	1584	
Gly	Arg	Val	Thr	Leu	Asp	Lys	Ser	Leu	Asn	Val	Ala	Tyr	Val	Asn	Glu		
		515					520					525					
tcc	agt	gcc	cta	tca	act	agc	caa	aaa	gcg	aca	tat	acc	ttt	act	gca	1632	
Ser	Ser	Ala	Leu	Ser	Thr	Ser	Gln	Lys	Ala	Thr	Tyr	Thr	Phe	Thr	Ala		
						535						540					
acg	gcg	ggc	aag	cca	ttg	aaa	atc	tcc	ctg	gta	tgg	tcg	gat	gcc	cct	1680	
Thr	Ala	Gly	Lys	Pro	Leu	Lys	Ile	Ser	Leu	Val	Trp	Ser	Asp	Ala	Pro		
545					550					555					560		

gca agc act act gct tct gta acc ctg gtc aat gat ttg gat ttg gtc 1728
 Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu Val
 565 570 575

att aca gca cca aac gga aca aga tat gtc ggg aat gac ttc tca gca 1776
 Ile Thr Ala Pro Asn Gly Thr Arg Tyr Val Gly Asn Asp Phe Ser Ala
 580 585 590

cca ttt gac aat aac tgg gat ggc cgc aat aac gta gaa aat gta ttt 1824
 Pro Phe Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val Phe
 595 600 605

att aat tcg ccc caa agt gga aca tat acc att gag gtg caa gca tat 1872
 Ile Asn Ser Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala Tyr
 610 615 620

aat gtg ccg gtt gga cca caa aac ttc tcg ttg gca att gtg aac taa 1920
 Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile Val Asn
 625 630 635

<210> 4

<211> 639

<212> PRT

<213> Bacillus sp.

<400> 4

Met Arg Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala Ile
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Leu Ser Thr Val Ala Leu Asn Asn Pro Ser Ala Gly Asp Ala Arg Thr
 20 25 30

Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Val Ser Gly
 35 40 45

Phe Ser Lys Gln Arg Gln Thr Gly Ala Ala Ala Phe Leu Val Glu Ser
 50 55 60

Glu Asn Val Lys Leu Leu Lys Gly Leu Leu Lys Lys Leu Glu Thr Val
 65 70 75 80

Pro Ala Asn Asn Lys Leu His Ile Val Gln Phe Asn Gly Pro Ile Leu
 85 90 95

Glu Glu Thr Lys Gln Lys Leu Glu Thr Thr Gly Ala Lys Ile Leu Asp
 100 105 110

Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val Gln
 115 120 125

Ser Lys Val Arg Ser Ile Glu His Val Glu Ser Val Glu Pro Tyr Leu
 130 135 140

Pro Lys Tyr Lys Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser Thr
 145 150 155 160

Leu Val Lys Ala Leu Ala Leu Asp Thr Lys Gln Asn Asn Lys Glu Val
 165 170 175

Gln Leu Arg Gly Ile Glu Glu Ile Ala Gln Tyr Val Ala Ser Asn Asp
 180 185 190

Val His Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp Val
 195 200 205

Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly Leu
 210 215 220

Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp Thr
 225 230 235 240

Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile Thr
 245 250 255

Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn Gly
 260 265 270

His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ala Thr Asn
 275 280 285

Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met Asp
 290 295 300

Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu Phe
 305 310 315 320

Ser Gln Ala Phe Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp Gly
 325 330 335

Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp Asp
 340 345 350

Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn Glu
 355 360 365
 Arg Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn Ala
 370 375 380
 Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser Tyr
 385 390 395 400
 Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro Thr
 405 410 415
 Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Tyr Ile
 420 425 430
 Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala Asn
 435 440 445
 His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr Pro
 450 455 460
 Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys Asn
 465 470 475 480
 Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile Ala
 485 490 495
 Gly Ala Ala Asp Val Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly Trp
 500 505 510
 Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn Glu
 515 520 525
 Ser Ser Ala Leu Ser Thr Ser Gln Lys Ala Thr Tyr Thr Phe Thr Ala
 530 535 540
 Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala Pro
 545 550 555 560
 Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu Val
 565 570 575
 Ile Thr Ala Pro Asn Gly Thr Arg Tyr Val Gly Asn Asp Phe Ser Ala
 580 585 590

Pro Phe Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val Phe
 595 600 605

Ile Asn Ser Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala Tyr
 610 615 620

Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile Val Asn
 625 630 635

<210> 5

<211> 1923

<212> DNA

<213> Bacillus sp.

<220>

<221> CDS

<222> (1) .. (1923)

<400> 5

atg aga aag aag aaa aag gtg ttt tta tct gtt tta tca gct gca gcg 48
 Met Arg Lys Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala
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att tgg tcg act gtt gcg tta agt aat cca tct gca ggt ggt gca agg 96
 Ile Leu Ser Thr Val Ala Leu Ser Asn Pro Ser Ala Gly Gly Ala Arg
 20 25 30

aat ttt gat ctg gat ttc aaa gga att cag aca aca act gat gct aaa 144
 Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Ala Lys
 35 40 45

ggt ttc tcc aag cag ggg cag act ggt gct gct gct ttt ctg gtg gaa 192
 Gly Phe Ser Lys Lys Gln Gly Gln Thr Gly Ala Ala Ala Phe Leu Val Glu
 50 55 60

tct gaa aat gtg aaa ctc cca aaa ggt ttg cag aag aag ctt gaa aca 240
 Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln Lys Lys Leu Glu Thr
 65 70 75 80

gtc ccg gca aat aat aaa ctc cat att atc caa ttc aat gga cca att 288
 Val Pro Ala Asn Asn Lys Leu His Ile Ile Gln Phe Asn Gly Pro Ile
 85 90 95

tta gaa gaa aca aaa cag cag ctg gaa aaa aca ggg gca aag att ctc 336
 Leu Glu Glu Thr Lys Lys Gln Gln Leu Glu Lys Thr Gly Ala Lys Ile Leu
 100 105 110

gac tac ata cct gat tat gct tac att gtc gag tat gag ggc gat gtt Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val 115 120 125	384
aag tca gca aca agc acc att gag cac gtg gaa tcc gtg gag cct tat Lys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr 130 135 140	432
ttg ccg ata tac aga ata gat ccc cag ctt ttc aca aaa ggg gca tca Leu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser 145 150 155 160	480
gag ctt gta aaa gca gtg gcg ctt gat aca aag cag aaa aat aaa gag Glu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu 165 170 175	528
gtg caa tta aga ggc atc gaa caa atc gca caa ttc gca ata agc aat Val Gln Leu Arg Gly Ile Glu Gln Ile Ala Gln Phe Ala Ile Ser Asn 180 185 190	576
gat gtg cta tat att acg gca aag cct gag tat aag gtg atg aat gat Asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp 195 200 205	624
gtt geg cgt gga att gtc aaa gcg gat gtg gct cag agc agc tac ggg Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly 210 215 220	672
ttg tat gga caa gga cag atc gta gcg gtt gcc gat aca ggg ctt gat Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp 225 230 235 240	720
aca ggt cgc aat gac agt tcg atg cat gaa gcc ttc cgc ggg aaa att Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile 245 250 255	768
act gca tta tat gca ttg gga cgg acg aat aat gcc aat gat acg aat Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn 260 265 270	816
ggt cat ggt acg cat gtg gct ggc tcc gta tta gga aac ggc tcc act Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ser Thr 275 280 285	864
aat aaa gga atg gcg cct cag gcg aat cta gtc ttc caa tct atc atg Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met 290 295 300	912
gat agc ggt ggg gga ctt gga gga cta cct tcg aat ctg caa acc tta Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu 305 310 315 320	960
ttc agc caa gca tac agt gct ggt gcc aga att cat aca aac tcc tgg Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp 325 330 335	1008
gga gca gca gtg aat ggg gct tac aca aca gat tcc aga aat gtg gat Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp 340 345 350	1056

gac tat gtg cgc aaa aat gat atg acg atc ctt ttc gct gcc ggg aat Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn 355 360 365	1104
gaa gga ccg aac ggc gga acc atc agt gca cca ggc aca gct aaa aat Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn 370 375 380	1152
gca ata aca gtc gga gct acg gaa aac ctc cgc cca agc ttt ggg tct Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser 385 390 395 400	1200
tat gcg gac aat atc aac cat gtg gca cag ttc tct tca cgt gga ccg Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro 405 410 415	1248
aca aag gat gga cgg atc aaa ccg gat gtc atg gca ccg gga acg ttc Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe 420 425 430	1296
ata cta tca gca aga tct tct ctt gca ccg gat tcc tcc ttc tgg gcg Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala 435 440 445	1344
aac cat gac agt aaa tat gca tac atg ggt gga acg tcc atg gct aca Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr 450 455 460	1392
ccg atc gtt gct gga aac gtg gca cag ctt cgt gag cat ttt gtg aaa Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys 465 470 475 480	1440
aac aga ggc atc aca cca aag cct tct cta tta aaa gcg gca ctg att Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile 485 490 495	1488
gcc ggt gca gct gac atc ggc ctt ggc tac ccg aac ggt aac caa gga Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly 500 505 510	1536
tgg gga cga gtg aca ttg gat aaa tcc ctg aac gtt gcc tat gtg aac Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn 515 520 525	1584
gag tcc agt tct cta tcc acc agc caa aaa gcg acg tac tcg ttt act Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe Thr 530 535 540	1632
gct act gcc ggc aag cct ttg aaa atc tcc ctg gta tgg tct gat gcc Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala 545 550 555 560	1680
cct gcg agc aca act gct tcc gta acg ctt gtc aat gat ctg gac ctt Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu 565 570 575	1728
gtc att acc gct cca aat ggc aca cag tat gta gga aat gac ttt act Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp Phe Thr 580 585 590	1776

tcg cca tac aat gat aac tgg gat ggc cgc aat aac gta gaa aat gta 1824
 Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val
 595 600 605

ttt att aat gca cca caa agc ggg acg tat aca att gag gta cag gct 1872
 Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala
 610 615 620

tat aac gta ccg gtt gga cca cag acc ttc tcg ttg gca att gtg aat 1920
 Tyr Asn Val Pro Val Gly Pro Gln Thr Phe Ser Leu Ala Ile Val Asn
 625 630 635 640

taa 1923

<210> 6

<211> 640

<212> PRT

<213> Bacillus sp.

<400> 6

Met Arg Lys Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala
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Ile Leu Ser Thr Val Ala Leu Ser Asn Pro Ser Ala Gly Gly Ala Arg
 20 25 30

Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Ala Lys
 35 40 45

Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala Phe Leu Val Glu
 50 55 60

Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln Lys Lys Leu Glu Thr
 65 70 75 80

Val Pro Ala Asn Asn Lys Leu His Ile Ile Gln Phe Asn Gly Pro Ile
 85 90 95

Leu Glu Glu Thr Lys Gln Gln Leu Glu Lys Thr Gly Ala Lys Ile Leu
 100 105 110

Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val
 115 120 125

Lys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr
 130 135 140

Leu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser
 145 150 155 160

Glu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu
 165 170 175

Val Gln Leu Arg Gly Ile Glu Gln Ile Ala Gln Phe Ala Ile Ser Asn
 180 185 190

Asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp
 195 200 205

Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly
 210 215 220

Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp
 225 230 235 240

Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile
 245 250 255

Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn
 260 265 270

Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ser Thr
 275 280 285

Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met
 290 295 300

Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu
 305 310 315 320

Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp
 325 330 335

Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp
 340 345 350

Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn
 355 360 365

Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn
 370 375 380

Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser
 385 390 395 400

Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro
 405 410 415

Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe
 420 425 430

Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala
 435 440 445

Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr
 450 455 460

Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys
 465 470 475 480

Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile
 485 490 495

Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly
 500 505 510

Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn
 515 520 525

Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe Thr
 530 535 540

Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala
 545 550 555 560

Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu
 565 570 575

Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp Phe Thr
 580 585 590

Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val
 595 600 605

Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala
610 615 620

Tyr Asn Val Pro Val Gly Pro Gln Thr Phe Ser Leu Ala Ile Val Asn
625 630 635 640

<210> 7

<211> 1923

<212> DNA

<213> Bacillus sp.

<220>

<221> CDS

<222> (1) .. (1923)

<400> 7

atg	aga	aag	aag	aaa	aag	gtg	ttt	tta	tct	ggt	tta	tca	gct	gca	gcg	48
Met	Arg	Lys	Lys	Lys	Lys	Val	Phe	Leu	Ser	Val	Leu	Ser	Ala	Ala	Ala	
1				5					10					15		

att	tgg	tcg	act	ggt	gcg	tta	agt	aat	cca	tct	gca	ggg	ggg	gca	agg	96
Ile	Leu	Ser	Thr	Val	Ala	Leu	Ser	Asn	Pro	Ser	Ala	Gly	Gly	Ala	Arg	
			20					25					30			

aat	ttt	gat	ctg	gat	ttc	aaa	gga	att	cag	aca	aca	act	gat	gct	aaa	144
Asn	Phe	Asp	Leu	Asp	Phe	Lys	Gly	Ile	Gln	Thr	Thr	Thr	Asp	Ala	Lys	
		35					40					45				

ggg	ttc	tcc	aag	cag	ggg	cag	act	ggg	gct	gct	gct	ttt	ctg	gtg	gaa	192
Gly	Phe	Ser	Lys	Gln	Gly	Gln	Thr	Gly	Ala	Ala	Ala	Phe	Leu	Val	Glu	
	50					55					60					

tct	gaa	aat	gtg	aaa	ctc	cca	aaa	ggg	ttg	cag	aag	aag	ctt	gaa	aca	240
Ser	Glu	Asn	Val	Lys	Leu	Pro	Lys	Gly	Leu	Gln	Lys	Lys	Leu	Glu	Thr	
65					70					75					80	

gtc	ccg	gca	aat	aat	aaa	ctc	cat	att	atc	caa	ttc	aat	gga	cca	att	288
Val	Pro	Ala	Asn	Asn	Lys	Leu	His	Ile	Ile	Gln	Phe	Asn	Gly	Pro	Ile	
				85					90						95	

tta	gaa	gaa	aca	aaa	cag	cag	ctg	gaa	aaa	aca	ggg	gca	aag	att	ctc	336
Leu	Glu	Glu	Thr	Lys	Gln	Gln	Leu	Glu	Lys	Thr	Gly	Ala	Lys	Ile	Leu	
			100					105						110		

gac	tac	ata	cct	gat	tat	gct	tac	att	gtc	gag	tat	gag	ggc	gat	gtt	384
Asp	Tyr	Ile	Pro	Asp	Tyr	Ala	Tyr	Ile	Val	Glu	Tyr	Glu	Gly	Asp	Val	
		115					120					125				

aag tca gca aca agc acc att gag cac gtg gaa tcc gtg gag cct tat	432
Lys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr	
130 135 140	
ttg ccg ata tac aga ata gat ccc cag ctt ttc aca aaa ggg gca tca	480
Leu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser	
145 150 155 160	
gag ctt gta aaa gca gtg gcg ctt gat aca aag cag aaa aat aaa gag	528
Glu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu	
165 170 175	
gtg caa tta aga ggc atc gaa caa atc gca caa ttc gca ata agc aat	576
Val Gln Leu Arg Gly Ile Glu Gln Ile Ala Gln Phe Ala Ile Ser Asn	
180 185 190	
gat gtg cta tat att acg gca aag cct gag tat aag gtg atg aat gat	624
Asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp	
195 200 205	
ggt gcg cgt gga att gtc aaa gcg gat gtg gct cag agc agc tac ggg	672
Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly	
210 215 220	
ttg tat gga caa gga cag atc gta gcg gtt gcc gat aca ggg ctt gat	720
Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp	
225 230 235 240	
aca ggt cgc aat gac agt tcg atg cat gaa gcc ttc cgc ggg aaa att	768
Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile	
245 250 255	
act gca tta tat gca ttg gga cgg acg aat aat gcc aat gat acg aat	816
Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn	
260 265 270	
ggt cat ggt acg cat gtg gct ggc tcc gta tta gga aac ggc tcc act	864
Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ser Thr	
275 280 285	
aat aaa gga atg gcg cct cag gcg aat cta gtc ttc caa tct atc atg	912
Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met	
290 295 300	
gat agc ggt ggg gga ctt gga gga cta cct tcg aat ctg caa acc tta	960
Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu	
305 310 315 320	
ttc agc caa gca tac agt gct ggt gcc aga att cat aca aac tcc tgg	1008
Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp	
325 330 335	
gga gca gca gtg aat ggg gct tac aca aca gat tcc aga aat gtg gat	1056
Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp	
340 345 350	
gac tat gtg cgc aaa aat gat atg acg atc ctt ttc gct gcc ggg aat	1104
Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn	
355 360 365	

gaa gga ccg aac ggc gga acc atc agt gca cca ggc aca gct aaa aat Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn 370 375 380	1152
gca ata aca gtc gga gct acg gaa aac ctc cgc cca agc ttt ggg tct Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser 385 390 395 400	1200
tat gcg gac aat atc aac cat gtg gca cag ttc tct tca cgt gga ccg Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro 405 410 415	1248
aca aag gat gga cgg atc aaa ccg gat gtc atg gca ccg gga acg ttc Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe 420 425 430	1296
ata cta tca gca aga tct tct ctt gca ccg gat tcc tcc ttc tgg gcg Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala 435 440 445	1344
aac cat gac agt aaa tat gca tac atg ggt gga acg tcc atg gct aca Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr 450 455 460	1392
ccg atc gtt gct gga aac gtg gca cag ctt cgt gag cat ttt gtg aaa Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys 465 470 475 480	1440
aac aga ggc atc aca cca aag cct tct cta tta aaa gcg gca ctg att Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile 485 490 495	1488
gcc ggt gca gct gac atc ggc ctt ggc tac ccg aac ggt aac caa gga Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly 500 505 510	1536
tgg gga cga gtg aca ttg gat aaa tcc ctg aac gtt gcc tat gtg aac Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn 515 520 525	1584
gag tcc agt tct cta tcc acc agc caa aaa gcg acg tac tcg ttt act Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe Thr 530 535 540	1632
gct act gcc ggc aag cct ttg aaa atc tcc ctg gta tgg tct gat gcc Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala 545 550 555 560	1680
cct gcg agc aca act gct tcc gta acg ctt gtc aat gat ctg gac ctt Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu 565 570 575	1728
gtc att acc gct cca aat ggc aca cag tat gta gga aat gac ttt act Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp Phe Thr 580 585 590	1776
tcg cca tac aat gat aac tgg gat ggc cgc aat aac gta gaa aat gta Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val 595 600 605	1824

ttt att aat gca cca caa agc ggg acg tat aca att gaa gta cag gct 1872
 phe ile asn ala pro gln ser gly thr tyr thr ile glu val gln ala
 610 615 620

aat aac gta ccg gtt gga cca cag aac ttc tcg ttg gca att gtg aat 1920
 tyr asn val pro val gly pro gln asn phe ser leu ala ile val asn
 525 630 635 640

taa 1923

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 <212> PRT
 <213> Bacillus sp.

<400> 8

Met Arg Lys Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala
 1 5 10 15

Ile Leu Ser Thr Val Ala Leu Ser Asn Pro Ser Ala Gly Gly Ala Arg
 20 25 30

Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Ala Lys
 35 40 45

Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala Phe Leu Val Glu
 50 55 60

Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln Lys Lys Leu Glu Thr
 65 70 75 80

Val Pro Ala Asn Asn Lys Leu His Ile Ile Gln Phe Asn Gly Pro Ile
 85 90 95

Leu Glu Glu Thr Lys Gln Gln Leu Glu Lys Thr Gly Ala Lys Ile Leu
 100 105 110

Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val
 115 120 125

Lys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr
 130 135 140

Leu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser
145 150 155 160

Glu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu
165 170 175

Val Gln Leu Arg Gly Ile Glu Gln Ile Ala Gln Phe Ala Ile Ser Asn
180 185 190

Asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp
195 200 205

Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly
210 215 220

Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp
225 230 235 240

Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile
245 250 255

Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn
260 265 270

Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ser Thr
275 280 285

Asp Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met
290 295 300

Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu
305 310 315 320

Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp
325 330 335

Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp
340 345 350

Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn
355 360 365

Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn
370 375 380

Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser
385 390 395 400

Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro
405 410 415

Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe
420 425 430

Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala
435 440 445

Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr
450 455 460

Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys
465 470 475 480

Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile
485 490 495

Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly
500 505 510

Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn
515 520 525

Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe Thr
530 535 540

Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala
545 550 555 560

Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu
565 570 575

Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp Phe Thr
580 585 590

Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val
595 600 605

Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala
610 615 620

Tyr	Asn	Val	Pro	Val	Gly	Pro	Gln	Asn	Phe	Ser	Leu	Ala	Ile	Val	Asn
625					630					635					640

<210> 9

<211> 20

<212> PRT

<213> Bacillus sp.

<400> 9

Asn	Asp	Val	Ala	Arg	His	Ile	Val	Lys	Ala	Asp	Val	Ala	Gln	Ser	Ser
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Tyr	Gly	Leu	Tyr
			20

<210> 10

<211> 14

<212> PRT

<213> Bacillus sp.

<400> 10

Gly	Ile	Val	Lys	Ala	Asp	Val	Ala	Gln	Ser	Ser	Tyr	Gly	Leu
1				5					10				

<210> 11

<211> 13

<212> PRT

<213> Bacillus sp.

<400> 11

Ile	Lys	Pro	Asp	Val	Met	Ala	Pro	Gly	Thr	Tyr	Ile	Leu
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<210> 12

<211> 20

<212> PRT

<213> Bacillus sp.

<400> 12

Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly
1 5 10 15

Ser Tyr Ala Asp
20

<210> 13

<211> 16

<212> PRT

<213> Bacillus sp.

<400> 13

Lys Asn Asp Met Val Ile Leu Phe Ala Ala Gly Asn Glu Gly Pro Asn
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<210> 14

<211> 24

<212> DNA

<213> Artificial/Unknown

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<223> n is a, g, c or t

<220>

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<222> (12)..(12)

<223> n is a, g, c or t

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<222> (18)..(18)

<223> n is a, g, c or t

<220>

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<222> (21)..(21)

<223> n is a, g, c or t

<400> 14

athgtgaarg cngaygtngc ncar

24

<210> 15

<211> 23

<212> DNA

<213> Artificial/Unknown

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<223> n is a, g, c or t

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<222> (15)..(15)

<223> n is a, g, c or t

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23

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<222> (21)..(21)

<223> n is a, g, c or t

<400> 16
athaarcng aygtnatggc ncc

23

<210> 17

<211> 24

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<223> n is a, g, c or t

<400> 17
tttrcgntadt gncanccncg ntgn

24

<210> 18

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<223> n is a, g, c or t

<400> 18
athacngtng gngcnacnga raa

23

<210> 19

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<212> DNA

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<400> 19
tttcttacc antadranaa rcg

23

<210> 20
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<223> n is a, g, c or t

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<221> misc_feature
<222> (18)..(18)
<223> n is a, g, c or t

<400> 20
aaygayatgg tnatgytnntt ygc 23

<210> 21
<211> 21
<212> DNA
<213> Artificial/Unknown

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<210> 22
<211> 21
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<213> Artificial/Unknown

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<223> Description of Artificial Sequence: primer

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tctggaatct gtcgtgtagg c

21

<210> 23

<211> 20

<212> DNA

<213> Artificial/Unknown

<220>

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<222> ()..()

<223> Description of Artificial Sequence: primer

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20

<210> 24

<211> 21

<212> DNA

<213> Artificial/Unknown

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<223> Description of Artificial Sequence: primer

<400> 24
ggaggcttgc cttccaatct g

21

SEQUENCE LISTING

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<120> Alkaline Protease

<130> FP-KS-0498

<150> JP 09-274570

<151> 1997-10-07

<160> 5

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<211> 639

<212> PRT

<213> *Bacillus sp.*

<220>

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148, 160, 165, 172, 183, 187, 188, 189, 194, 286, 306, 324, 369, 431, 501,
531, 541, 584, 591, 592, 594, 595, 596, 611, 632

<223> Xaa=arbitraty amino acid

<400>

Met Arg Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala Ile

1 5 10 15

Leu Ser Thr Val Ala Leu Xaa Asn Pro Ser Ala Gly Xaa Ala Arg Xaa

20 25 30

Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Xaa Xaa Gly

35 40 45

Phe Ser Lys Gln Xaa Gln Thr Gly Ala Ala Ala Phe Leu Val Glu Ser

50 55 60

Glu Asn Val Lys Leu Xaa Lys Gly Leu Xaa Lys Lys Leu Glu Thr Val

65 70 75 80

Pro Ala Asn Asn Lys Leu His Ile Xaa Gln Phe Asn Gly Pro Ile Leu

85 90 95

Glu Glu Thr Lys Gln Xaa Leu Glu Xaa Thr Gly Ala Lys Ile Leu Asp

100 105 110

Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val Xaa

115 120 125

Ser Xaa Xaa Xaa Xaa Ile Glu His Val Glu Ser Val Glu Pro Tyr Leu

130 135 140

Pro Xaa Tyr Xaa Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser Xaa

145 150 155 160

Leu Val Lys Ala Xaa Ala Leu Asp Thr Lys Gln Xaa Asn Lys Glu Val

165 170 175

Gln Leu Arg Gly Ile Glu Xaa Ile Ala Gln Xaa Xaa Xaa Ser Asn Asp

180 185 190

Val Xaa Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp Val

195 200 205

Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly Leu

210

215

220

Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp Thr

225

230

235

240

Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile Thr

245

250

255

Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn Gly

260

265

270

His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Xaa Thr Asn

275

280

285

Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met Asp

290

295

300

Ser Xaa Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu Phe

305

310

315

320

Ser Gln Ala Xaa Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp Gly

325

330

335

Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp Asp

340

345

350

Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn Glu

355

360

365

Xaa Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn Ala

370

375

380

Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser Tyr

385

390

395

400

Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro Thr

405

410

415

Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Xaa Ile

420

425

430

Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala Asn

435

440

445

His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr Pro

450

455

460

Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys Asn

465

470

475

480

Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile Ala

485

490

495

Gly Ala Ala Asp Xaa Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly Trp

500

505

510

Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn Glu

515

520

525

Ser Ser Xaa Leu Ser Thr Ser Gln Lys Ala Thr Tyr Xaa Phe Thr Ala

530

535

540

Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala Pro

545

550

555

560

Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu Val

565

570

575

Ile Thr Ala Pro Asn Gly Thr Xaa Tyr Val Gly Asn Asp Phe Xaa Xaa

580

585

590

Pro Xaa Xaa Xaa Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val Phe

595

600

605

Ile Asn Xaa Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala Tyr

610

615

620

Asn Val Pro Val Gly Pro Gln Xaa Phe Ser Leu Ala Ile Val Asn

625 630 635

<210> 2

<211> 640

<212> PRT

<213> *Bacillus sp.*

<220>

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149, 161, 166, 173, 184, 188, 189, 190, 195, 287, 307, 325, 370, 432, 502,
532, 542, 585, 592, 593, 595, 596, 597, 612, 633

<223> Xaa=arbitrary amino acid

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Met Arg Xaa Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala

1 5 10 15

Ile Leu Ser Thr Val Ala Leu Xaa Asn Pro Ser Ala Gly Xaa Ala Arg

20 25 30

Xaa Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Xaa Xaa

35 40 45

Gly Phe Ser Lys Gln Xaa Gln Thr Gly Ala Ala Ala Phe Leu Val Glu

50 55 60

Ser Glu Asn Val Lys Leu Xaa Lys Gly Leu Xaa Lys Lys Leu Glu Thr

65 70 75 80

Val Pro Ala Asn Asn Lys Leu His Ile Xaa Gln Phe Asn Gly Pro Ile

	85	90	95
Leu Glu Glu Thr Lys Gln Xaa	Leu Glu Xaa Thr Gly Ala Lys Ile Leu		
100	105	110	
Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val			
115	120	125	
Xaa Ser Xaa Xaa Xaa Xaa Ile Glu His Val Glu Ser Val Glu Pro Tyr			
130	135	140	
Leu Pro Xaa Tyr Xaa Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser			
145	150	155	160
Xaa Leu Val Lys Ala Xaa Ala Leu Asp Thr Lys Gln Xaa Asn Lys Glu			
165	170	175	
Val Gln Leu Arg Gly Ile Glu Xaa Ile Ala Gln Xaa Xaa Xaa Ser Asn			
180	185	190	
Asp Val Xaa Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp			
195	200	205	
Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly			
210	215	220	
Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp			
225	230	235	240
Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile			
245	250	255	
Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn			
260	265	270	
Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Xaa Thr			
275	280	285	
Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met			

290	295	300	
Asp Ser Xaa Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu			
305	310	315	320
Phe Ser Gln Ala Xaa Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp			
	325	330	335
Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp			
	340	345	350
Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn			
	355	360	365
Glu Xaa Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn			
	370	375	380
Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser			
385	390	395	400
Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro			
	405	410	415
Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Xaa			
	420	425	430
Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala			
	435	440	445
Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr			
	450	455	460
Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys			
465	470	475	480
Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile			
	485	490	495
Ala Gly Ala Ala Asp Xaa Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly			

500 505 510
 Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn
 515 520 525
 Glu Ser Ser Xaa Leu Ser Thr Ser Gln Lys Ala Thr Tyr Xaa Phe Thr
 530 535 540
 Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala
 545 550 555 560
 Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu
 565 570 575
 Val Ile Thr Ala Pro Asn Gly Thr Xaa Tyr Val Gly Asn Asp Phe Xaa
 580 585 590
 Xaa Pro Xaa Xaa Xaa Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val
 595 600 605
 Phe Ile Asn Xaa Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala
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 Tyr Asn Val Pro Val Gly Pro Gln Xaa Phe Ser Leu Ala Ile Val Asn
 625 630 635 640

<210> 3

<211> 1920

<212> DNA

<213> *Bacillus sp.*

<400>

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 Met Arg Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala Ile

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ctg	tcg	act	ggt	gca tta aac aat ccc tcg gct ggt gat gca agg act 96
Leu	Ser	Thr	Val	Ala Leu Asn Asn Pro Ser Ala Gly Asp Ala Arg Thr
	20	25	30	
ttt	gat	ctg	gat	ttt aaa gga att caa aca aca acc gat gtc agt ggt 144
Phe	Asp	Leu	Asp	Phe Lys Gly Ile Gln Thr Thr Thr Asp Val Ser Gly
	35	40	45	
ttc	tcc	aaa	cag	cga caa aca ggt gcg gct gca ttt ctg gtg gag tct 192
Phe	Ser	Lys	Gln	Arg Gln Thr Gly Ala Ala Ala Phe Leu Val Glu Ser
	50	55	60	
gaa	aat	gtg	aaa	ctt ctt aaa gga ttg cta aag aaa ctt gaa aca gta 240
Glu	Asn	Val	Lys	Leu Leu Lys Gly Leu Leu Lys Lys Leu Glu Thr Val
65		70	75	80
ccg	gca	aat	aat	aaa ctc cat att gtc caa ttc aat ggc ccc att tta 288
Pro	Ala	Asn	Asn	Lys Leu His Ile Val Gln Phe Asn Gly Pro Ile Leu
	85	90	95	
gaa	gaa	aca	aaa	cag aag cta gag aca act gga gca aag att ctc gac 336
Glu	Glu	Thr	Lys	Gln Lys Leu Glu Thr Thr Gly Ala Lys Ile Leu Asp
	100	105	110	
tac	atc	cct	gat	tat gca tat att gtc gag tat gag ggg gat gtt cag 384
Tyr	Ile	Pro	Asp	Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val Gln
	115	120	125	
tca	aaa	gtc	cg	tcc att gaa cac gtg gaa tca gtg gag cca tac ttg 432
Ser	Lys	Val	Arg	Ser Ile Glu His Val Glu Ser Val Glu Pro Tyr Leu
	130	135	140	
ccg	aaa	tac	aaa	ata gat ccc cag ctt ttc aca aaa ggc gca tcg acg 480

Pro Lys Tyr Lys Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser Thr
 145 150 155 160
 ctg gtg aaa gcg ttg gcg ctt gat acg aag cag aac aat aaa gaa gtg 528
 Leu Val Lys Ala Leu Ala Leu Asp Thr Lys Gln Asn Asn Lys Glu Val
 165 170 175
 caa tta aga ggc atc gag gaa atc gct cag tac gta gca agc aat gac 576
 Gln Leu Arg Gly Ile Glu Glu Ile Ala Gln Tyr Val Ala Ser Asn Asp
 180 185 190
 gtc cat tat att acg gca aag cct gaa tat aag gtg atg aat gat gtg 624
 Val His Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp Val
 195 200 205
 gcc aga ggt att gtc aaa gcg gat gtg gca cag agc agc tac ggt ttg 672
 Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly Leu
 210 215 220
 tat gga caa ggc cag att gtc gca gtt gcc gat act gga ttg gat aca 720
 Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp Thr
 225 230 235 240
 gga aga aac gac agt tcg atg cat gaa gcc ttc cgc ggt aaa ata aca 768
 Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile Thr
 245 250 255
 gca cta tat gca ctg ggt cgg acg aat aat gcg aat gat acg aac ggt 816
 Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn Gly
 260 265 270
 cat ggt acc cat gtg gca ggt tcg gta tta gga aat ggc gca acg aat 864
 His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ala Thr Asn
 275 280 285

aaa gga atg gca cct caa gcg aat ctg gtt ttt caa tcc atc atg gat 912

Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met Asp

290

295

300

agc agt ggt ggg ctt gga ggc ttg cct tcc aat ctg caa acc tta ttc 960

Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu Phe

305

310

315

320

agc caa gca ttc agt gca ggt gcc aga att cat aca aac tcc tgg ggg 1008

Ser Gln Ala Phe Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp Gly

325

330

335

gca gcg gtg aat ggg gcc tac acg aca gat tcc aga aat gtg gat gac 1056

Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp Asp

340

345

350

tat gta agg aaa aat gat atg acg att ctt ttc gcg gct ggg aat gaa 1104

Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn Glu

355

360

365

agg ccg aac ggc ggt acc atc agt gca cct ggt acg gct aaa aac gcc 1152

Arg Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn Ala

370

375

380

ata aca gtc ggc gca acc gaa aac ctg cgt cca agc ttc ggt tcc tat 1200

Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser Tyr

385

390

395

400

gca gat aat att aac cac gtt gca cag ttc tct tcc cgt ggc ccg aca 1248

Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro Thr

405

410

415

aaa gat ggg cga atc aag cct gat gtc atg gcg cca ggg aca tac att 1296

Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Tyr Ile

420 425 430
 tta tca gca aga tct tct ctt gca ccc gat tcc tcc ttc tgg gcg aat 1344
 Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala Asn
 435 440 445
 cat gac agc aaa tat gcc tat atg ggt gga acg tcc atg gca aca ccg 1392
 His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr Pro
 450 455 460
 att gtt gcg ggg aat gtt gca cag ctc cgt gag cat ttt gtg aaa aat 1440
 Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys Asn
 465 470 475 480
 aga gga atc act cct aag cct tcc cta ttg aaa gca gct ttg att gca 1488
 Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile Ala
 485 490 495
 ggt gct gct gat gtt gga ttg ggt tat ccg aac gga aac caa gga tgg 1536
 Gly Ala Ala Asp Val Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly Trp
 500 505 510
 ggc cga gtg acc ctg gat aaa tcg ttg aac gtt gcc tat gtg aac gaa 1584
 Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn Glu
 515 520 525
 tcc agt gcc cta tca act agc caa aaa gcg aca tat acc ttt act gca 1632
 Ser Ser Ala Leu Ser Thr Ser Gln Lys Ala Thr Tyr Thr Phe Thr Ala
 530 535 540
 acg gcg ggc aag cca ttg aaa atc tcc ctg gta tgg tcg gat gcc cct 1680
 Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala Pro
 545 550 555 560
 gca agc act act gct tct gta acc ctg gtc aat gat ttg gat ttg gtc 1728

Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu Val

565

570

575

att aca gca cca aac gga aca aga tat gtc ggg aat gac ttc tca gca 1776

Ile Thr Ala Pro Asn Gly Thr Arg Tyr Val Gly Asn Asp Phe Ser Ala

580

585

590

cca ttt gac aat aac tgg gat ggc cgc aat aac gta gaa aat gta ttt 1824

Pro Phe Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val Phe

595

600

605

att aat tcg ccc caa agt gga aca tat acc att gag gtg caa gca tat 1872

Ile Asn Ser Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala Tyr

610

615

620

aat gtg ccg gtt gga cca caa aac ttc tcg ttg gca att gtg aac taa 1920

Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile Val Asn

625

630

635

<210> 4

<211> 1923

<212> DNA

<213> *Bacillus sp.*

<400>

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Met Arg Lys Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala

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10

15

att ttg tcg act gtt gcg tta agt aat cca tct gca ggt ggt gca agg 96

Ile Leu Ser Thr Val Ala Leu Ser Asn Pro Ser Ala Gly Gly Ala Arg

	20	25	30	
	aat ttt gat ctg gat ttc aaa gga att cag aca aca act gat gct aaa			144
	Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Ala Lys			
	35	40	45	
	ggt ttc tcc aag cag ggg cag act ggt gct gct gct ttt ctg gtg gaa			192
	Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala Phe Leu Val Glu			
	50	55	60	
	tct gaa aat gtg aaa ctc cca aaa ggt ttg cag aag aag ctt gaa aca			240
	Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln Lys Lys Leu Glu Thr			
	65	70	75	80
	gtc ccg gca aat aat aaa ctc cat att atc caa ttc aat gga cca att			288
	Val Pro Ala Asn Asn Lys Leu His Ile Ile Gln Phe Asn Gly Pro Ile			
	85	90	95	
	tta gaa gaa aca aaa cag cag ctg gaa aaa aca ggg gca aag att ctc			336
	Leu Glu Glu Thr Lys Gln Gln Leu Glu Lys Thr Gly Ala Lys Ile Leu			
	100	105	110	
	gac tac ata cct gat tat gct tac att gtc gag tat gag ggc gat gtt			384
	Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val			
	115	120	125	
	aag tca gca aca agc acc att gag cac gtg gaa tcc gtg gag cct tat			432
	Lys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr			
	130	135	140	
	ttg ccg ata tac aga ata gat ccc cag ctt ttc aca aaa ggg gca tca			480
	Leu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser			
	145	150	155	160
	gag ctt gta aaa gca gtg gcg ctt gat aca aag cag aaa aat aaa gag			528

Glu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu

165

170

175

gtg caa tta aga ggc atc gaa caa atc gca caa ttc gca ata agc aat 576

Val Gln Leu Arg Gly Ile Glu Gln Ile Ala Gln Phe Ala Ile Ser Asn

180

185

190

gat gtg cta tat att acg gca aag cct gag tat aag gtg atg aat gat 624

Asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp

195

200

205

gtt gcg cgt gga att gtc aaa gcg gat gtg gct cag agc agc tac ggg 672

Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly

210

215

220

ttg tat gga caa gga cag atc gta gcg gtt gcc gat aca ggg ctt gat 720

Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp

225

230

235

240

aca ggt cgc aat gac agt tcg atg cat gaa gcc ttc cgc ggg aaa att 768

Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile

245

250

255

act gca tta tat gca ttg gga cgg acg aat aat gcc aat gat acg aat 816

Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn

260

265

270

ggc cat ggt acg cat gtg gct ggc tcc gta tta gga aac ggc tcc act 864

Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ser Thr

275

280

285

aat aaa gga atg gcg cct cag gcg aat cta gtc ttc caa tct atc atg 912

Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met

290

295

300

gat agc ggt ggg gga ctt gga gga cta cct tcg aat ctg caa acc tta 960

Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu

305 310 315 320

ttc agc caa gca tac agt gct ggt gcc aga att cat aca aac tcc tgg 1008

Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp

325 330 335

gga gca gca gtg aat ggg gct tac aca aca gat tcc aga aat gtg gat 1056

Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp

340 345 350

gac tat gtg cgc aaa aat gat atg acg atc ctt ttc gct gcc ggg aat 1104

Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn

355 360 365

gaa gga ccg aac ggc gga acc atc agt gca cca ggc aca gct aaa aat 1152

Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn

370 375 380

gca ata aca gtc gga gct acg gaa aac ctc cgc cca agc ttt ggg tct 1200

Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser

385 390 395 400

tat gcg gac aat atc aac cat gtg gca cag ttc tct tca cgt gga ccg 1248

Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro

405 410 415

aca aag gat gga cgg atc aaa ccg gat gtc atg gca ccg gga acg ttc 1296

Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe

420 425 430

ata cta tca gca aga tct tct ctt gca ccg gat tcc tcc ttc tgg gcg 1344

Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala

435 440 445
 aac cat gac agt aaa tat gca tac atg ggt gga acg tcc atg gct aca 1392
 Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr
 450 455 460
 ccg atc gtt gct gga aac gtg gca cag ctt cgt gag cat ttt gtg aaa 1440
 Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys
 465 470 475 480
 aac aga ggc atc aca cca aag cct tct cta tta aaa gcg gca ctg att 1488
 Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile
 485 490 495
 gcc ggt gca gct gac atc ggc ctt ggc tac ccg aac ggt aac caa gga 1536
 Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly
 500 505 510
 tgg gga cga gtg aca ttg gat aaa tcc ctg aac gtt gcc tat gtg aac 1584
 Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn
 515 520 525
 gag tcc agt tct cta tcc acc agc caa aaa gcg acg tac tcg ttt act 1632
 Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe Thr
 530 535 540
 gct act gcc ggc aag cct ttg aaa atc tcc ctg gta tgg tct gat gcc 1680
 Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala
 545 550 555 560
 cct gcg agc aca act gct tcc gta acg ctt gtc aat gat ctg gac ctt 1728
 Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu
 565 570 575
 gtc att acc gct cca aat ggc aca cag tat gta gga aat gac ttt act 1776

Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp Phe Thr

580

585

590

tcg cca tac aat gat aac tgg gat ggc cgc aat aac gta gaa aat gta 1824

Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val

595

600

605

ttt att aat gca cca caa agc ggg acg tat aca att gag gta cag gct 1872

Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala

610

615

620

tat aac gta ccg gtt gga cca cag acc ttc tcg ttg gca att gtg aat 1920

Tyr Asn Val Pro Val Gly Pro Gln Thr Phe Ser Leu Ala Ile Val Asn

625

630

635

640

taa

1923

<210> 5

<211> 1923

<212> DNA

<212> *Bacillus sp.*

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10

15

att ttg tcg act gtt gcg tta agt aat cca tct gca ggt ggt gca agg 96

Ile Leu Ser Thr Val Ala Leu Ser Asn Pro Ser Ala Gly Gly Ala Arg

20

25

30

aat ttt gat ctg gat ttc aaa gga att cag aca aca act gat gct aaa 144

Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Ala Lys

35

40

45

ggt ttc tcc aag cag ggg cag act ggt gct gct gct ttt ctg gtg gaa 192

Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala Phe Leu Val Glu

50

55

60

tct gaa aat gtg aaa ctc cca aaa ggt ttg cag aag aag ctt gaa aca 240

Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln Lys Lys Leu Glu Thr

65

70

75

80

gtc ccg gca aat aat aaa ctc cat att atc caa ttc aat gga cca att 288

Val Pro Ala Asn Asn Lys Leu His Ile Ile Gln Phe Asn Gly Pro Ile

85

90

95

tta gaa gaa aca aaa cag cag ctg gaa aaa aca ggg gca aag att ctc 336

Leu Glu Glu Thr Lys Gln Gln Leu Glu Lys Thr Gly Ala Lys Ile Leu

100

105

110

gac tac ata cct gat tat gct tac att gtc gag tat gag ggc gat gtt 384

Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val

115

120

125

aag tca gca aca agc acc att gag cac gtg gaa tcc gtg gag cct tat 432

Lys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr

130

135

140

ttg ccg ata tac aga ata gat ccc cag ctt ttc aca aaa ggg gca tca 480

Leu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser

145

150

155

160

gag ctt gta aaa gca gtg gcg ctt gat aca aag cag aaa aat aaa gag 528

Glu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu

165

170

175

gtg caa tta aga ggc atc gaa caa atc gca caa ttc gca ata agc aat 576

Val Gln Leu Arg Gly Ile Glu Gln Ile Ala Gln Phe Ala Ile Ser Asn

180

185

190

gat gtg cta tat att acg gca aag cct gag tat aag gtg atg aat gat 624

Asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp

195

200

205

gtt gcg cgt gga att gtc aaa gcg gat gtg gct cag agc agc tac ggg 672

Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly

210

215

220

ttg tat gga caa gga cag atc gta gcg gtt gcc gat aca ggg ctt gat 720

Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp

225

230

235

240

aca ggt cgc aat gac agt tcg atg cat gaa gcc ttc cgc ggg aaa att 768

Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile

245

250

255

act gca tta tat gca ttg gga cgg acg aat aat gcc aat gat acg aat 816

Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn

260

265

270

ggt cat ggt acg cat gtg gct ggc tcc gta tta gga aac ggc tcc act 864

Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ser Thr

275

280

285

aat aaa gga atg gcg cct cag gcg aat cta gtc ttc caa tct atc atg 912

Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met

290

295

300

gat agc ggt ggg gga ctt gga gga cta cct tcg aat ctg caa acc tta 960

Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu

305 310 315 320
 ttc agc caa gca tac agt gct ggt gcc aga att cat aca aac tcc tgg 1008
 Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp
 325 330 335
 gga gca gca gtg aat ggg gct tac aca aca gat tcc aga aat gtg gat 1056
 Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp
 340 345 350
 gac tat gtg cgc aaa aat gat atg acg atc ctt ttc gct gcc ggg aat 1104
 Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn
 355 360 365
 gaa gga ccg aac ggc gga acc atc agt gca cca ggc aca gct aaa aat 1152
 Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn
 370 375 380
 gca ata aca gtc gga gct acg gaa aac ctc cgc cca agc ttt ggg tct 1200
 Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser
 385 390 395 400
 tat gcg gac aat atc aac cat gtg gca cag ttc tct tca cgt gga ccg 1248
 Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro
 405 410 415
 aca aag gat gga cgg atc aaa ccg gat gtc atg gca ccg gga acg ttc 1296
 Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe
 420 425 430
 ata cta tca gca aga tct tct ctt gca ccg gat tcc tcc ttc tgg gcg 1344
 Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala
 435 440 445
 aac cat gac agt aaa tat gca tac atg ggt gga acg tcc atg gct aca 1392

Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr

450

455

460

ccg atc gtt gct gga aac gtg gca cag ctt cgt gag cat ttt gtg aaa 1440

Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys

465

470

475

480

aac aga ggc atc aca cca aag cct tct cta tta aaa gcg gca ctg att 1488

Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile

485

490

495

gcc ggt gca gct gac atc ggc ctt ggc tac ccg aac ggt aac caa gga 1536

Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly

500

505

510

tgg gga cga gtg aca ttg gat aaa tcc ctg aac gtt gcc tat gtg aac 1584

Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn

515

520

525

gag tcc agt tct cta tcc acc agc caa aaa gcg acg tac tcg ttt act 1632

Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe Thr

530

535

540

gct act gcc ggc aag cct ttg aaa atc tcc ctg gta tgg tct gat gcc 1680

Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala

545

550

555

560

cct gcg agc aca act gct tcc gta acg ctt gtc aat gat ctg gac ctt 1728

Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu

565

570

575

gtc att acc gct cca aat ggc aca cag tat gta gga aat gac ttt act 1776

Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp Phe Thr

580

585

590

tcg cca tac aat gat aac tgg gat ggc cgc aat aac gta gaa aat gta 1824

Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val

595

600

605

ttt att aat gca cca caa agc ggg acg tat aca att gaa gta cag gct 1872

Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala

610

615

620

tat aac gta ccg gtt gga cca cag aac ttc tcg ttg gca att gtg aat 1920

Tyr Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile Val Asn

625

630

635

640

taa

1923